

In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-17 in the above-captioned application. A substitute computer readable form (CRF) copy accompanies this response.

**AMENDMENTS**

In the Specification:

Please replace the paragraph beginning at page 29, line 18, with the following rewritten paragraph:

--Additional illustrative embodiments of the invention disclosed herein include 20P1F12/TMPRSS2 polypeptides containing the amino acid residues of one or more of the biological motifs contained within the 20P1F12/TMPRSS2 polypeptide sequence as shown in FIG. 1 (and the polynucleotides encoding these polypeptides). In one embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 N-glycosylation sites such as NTSA at residues 213-216 and/or NSSR at residues 249-252. In another embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 Protein Kinase C phosphorylation sites such as TSK at residues 78-80, TSK at residues 447-449, TKK at residues 81-83, SQR at residues 163-165, SSK at residues 232-234, SLR at residues 238-240, SSR at residues 250-252, and/or TQR at residues 407-409. In another embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 casein kinase II phosphorylation sites such as TVYE at residues 35-38, SGIE at residues 116-119 and/or TFND at residues 356-359. In another embodiment, typical polypeptides of the invention can contain one or more of the N-myristoylation sites such as GSPPAI (SEQ ID NO: 30) at residues 6-11, GTVCTS (SEQ ID NO: 31) at residues 74-79, GAALAA (SEQ ID NO: 32) at residues 97-102, GSKCSN (SEQ ID NO: 33) at residues 110-115, GVNLS (SEQ ID NO: 34) at residues 245-250, GGESAL (SEQ ID NO: 35) at residues 258-263, GNVDSC (SEQ ID NO: 36) at residues 432-437, GSGCAK (SEQ ID NO: 37) at residues 462-467, GCAKAY (SEQ ID NO: 38) at residues 464-469 and/or GVYGN (SEQ ID

C2 NO: 39) at residues 472-477. In another embodiment, typical polypeptides of the invention can contain the ATP/GTP-binding site motif A (P-loop), ATEEKGKT (SEQ ID NO: 40) at residues 386-393. In another embodiment, typical polypeptides of the invention can contain the LDL-receptor class A (LDLRA) domain signature CINPSNWCDGVSHCPGGEDENRC (SEQ ID NO: 41) at residues 126-148. In another embodiment, typical polypeptides of the invention can contain the Serine proteases, trypsin family, histidine active site VTAAHC (SEQ ID NO: 42) at residues 292-297. In another embodiment, typical polypeptides of the invention can contain the Serine proteases, trypsin family, serine active site DSCQGDSGGPLV (SEQ ID NO: 43) at residues 435-446. Related embodiments of these inventions include polypeptides containing combinations of the different motifs discussed above with preferable embodiments being those which contain no insertions, deletions or substitutions either within the motifs or the intervening sequences of these polypeptides.--

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